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BOUWMEESTER, ANTONIUS
ROYET, JULIEN

<130> 55880 (71745)

<140> 09/830,980

<141> 2001-05-02

<150> PCT/IB99/01891

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<150> GB 9824045.0

<151> 1998-11-03

<160> 16

<170> PatentIn Ver. 2.1

<210> 1

<211> 480

<212> PRT

<213> Drosophila sp.

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Ala Arg Leu Val Tyr Thr Gly Glu Glu Ala Gly Pro Pro Ile Asp Leu
20 25 30

Pro Ala Gly Ile Thr Thr Gln Gln Leu Gly Leu Ile Cys Asn Ala Leu
35 40 45

Leu Lys Asn Glu Glu Ala Thr Pro Tyr Leu Phe Phe Val Gly Glu Asp
50 55 60

Glu Ile Lys Lys Ser Leu Glu Asp Thr Leu Asp Leu Ala Ser Val Asp
65 70 75 80

Thr Glu Asn Val Ile Asp Ile Val Tyr Gln Pro Gln Ala Val Phe Lys
85 90 95

Val Arg Pro Val Thr Arg Cys Thr Ser Ser Met Pro Gly His Ala Glu
100 105 110

Ala Val Val Ser Leu Asn Phe Ser Pro Asp Gly Ala His Leu Ala Ser
115 120 125

Gly Ser Gly Asp Thr Thr Val Arg Leu Trp Asp Leu Asn Thr Glu Thr
130 135 140

Pro 145	His	Phe	Thr	Cys	Thr 150	Gly	His	Lys	Gln	Trp 155	Val	Leu	Cys	Val	Ser 160
Trp	Ala	Pro	Asp	Gly 165	Lys	Arg	Leu	Ala	Ser 170	Gly	Cys	Lys	Ala	Gly 175	Ser
Ile	Ile	Ile	Trp 180	Asp	Pro	Glu	Thr	Gly 185	Gln	Gln	Lys	Gly	Arg 190	Pro	Leu
Ser	Gly	His 195	Lys	Lys	His	Ile	Asn 200	Cys	Leu	Ala	Trp	Glu 205	Pro	Tyr	His
Arg	Asp 210	Pro	Glu	Cys	Arg	Lys 215	Leu	Ala	Ser	Ala	Ser 220	Gly	Asp	Gly	Asp
Cys 225	Arg	Ile	Trp	Asp	Val 230	Lys	Leu	Gly	Gln	Cys 235	Leu	Met	Asn	Ile	Ala 240
Gly	His	Thr	Asn 245	Ala	Val	Thr	Ala	Val	Arg 250	Trp	Gly	Gly	Ala	Gly 255	Leu
Ile	Tyr	Thr	Ser 260	Ser	Lys	Asp	Arg 265	Thr	Val	Lys	Met	Trp 270	Arg	Ala	Ala
Asp	Gly	Ile 275	Leu	Cys	Arg	Thr	Phe 280	Ser	Gly	His	Ala	His 285	Trp	Val	Asn
Asn 290	Ile	Ala	Leu	Ser	Thr	Asp 295	Tyr	Val	Leu	Arg	Thr 300	Gly	Pro	Phe	His
Pro 305	Val	Lys	Asp	Arg	Ser 310	Lys	Ser	His	Leu	Ser 315	Leu	Ser	Thr	Glu	Glu 320
Leu	Gln	Glu	Ser	Ala 325	Leu	Lys	Arg	Tyr	Gln 330	Ala	Val	Cys	Pro	Asp 335	Glu
Val	Glu	Ser	Leu 340	Val	Ser	Cys	Ser 345	Asp	Asp	Asn	Thr	Leu 350	Tyr	Leu	Trp
Arg	Asn	Asn 355	Gln	Asn	Lys	Cys	Val 360	Glu	Arg	Met	Thr	Gly 365	His	Gln	Asn
Val 370	Val	Asn	Asp	Val	Lys	Tyr 375	Ser	Pro	Asp	Val	Lys 380	Leu	Ile	Ala	Ser
Ala 385	Ser	Phe	Asp	Lys	Ser 390	Val	Arg	Leu	Trp	Arg 395	Ala	Ser	Asp	Gly	Gln 400
Tyr	Met	Ala	Thr 405	Phe	Arg	Gly	His	Val	Gln 410	Ala	Val	Tyr	Thr	Val 415	Ala
Trp	Ser	Ala	Asp 420	Ser	Arg	Leu	Ile 425	Val	Ser	Gly	Ser	Lys	Asp 430	Ser	Thr
Leu	Lys	Val 435	Trp	Ser	Val	Gln	Thr 440	Lys	Lys	Leu	Ala	Gln 445	Glu	Leu	Pro

Gly His Ala Asp Glu Val Phe Gly Val Asp Trp Ala Pro Asp Gly Ser
 450 455 460

Arg Val Ala Ser Gly Gly Lys Asp Lys Val Ile Lys Leu Trp Ala Tyr
 465 470 475 480

<210> 2

<211> 1555

<212> DNA

<213> Drosophila sp.

<400> 2

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<211> 513

<212> PRT

<213> Saccharomyces cerevisiae

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Gln Leu Pro Arg Glu Val Ala Ile Ile Pro Lys Asp Leu Pro Asn Val
 20 25 30

Ser Ile Lys Phe Gln Ala Leu Asp Thr Gly Asp Asn Val Gly Gly Ala
 35 40 45

Leu	Arg	Val	Pro	Gly	Ala	Ile	Ser	Glu	Lys	Gln	Leu	Glu	Glu	Leu	Leu
50						55					60				
Asn	Gln	Leu	Asn	Gly	Thr	Ser	Asp	Asp	Pro	Val	Pro	Tyr	Thr	Phe	Ser
65					70					75					80
Cys	Thr	Ile	Gln	Gly	Lys	Lys	Ala	Ser	Asp	Pro	Val	Lys	Thr	Ile	Asp
				85					90					95	
Ile	Thr	Asp	Asn	Leu	Tyr	Ser	Ser	Leu	Ile	Lys	Pro	Gly	Tyr	Asn	Ser
			100					105					110		
Thr	Glu	Asp	Gln	Ile	Thr	Leu	Leu	Tyr	Thr	Pro	Arg	Ala	Val	Phe	Lys
		115					120					125			
Val	Lys	Pro	Val	Thr	Arg	Ser	Ser	Ser	Ala	Ile	Ala	Gly	His	Gly	Ser
		130				135					140				
Thr	Ile	Leu	Cys	Ser	Ala	Phe	Ala	Pro	His	Thr	Ser	Ser	Arg	Met	Val
145					150					155					160
Thr	Gly	Ala	Gly	Asp	Asn	Thr	Ala	Arg	Ile	Trp	Asp	Cys	Asp	Thr	Gln
				165					170					175	
Thr	Pro	Met	His	Thr	Leu	Lys	Gly	His	Tyr	Asn	Trp	Val	Leu	Cys	Val
			180					185					190		
Ser	Trp	Ser	Pro	Asp	Gly	Glu	Val	Ile	Ala	Thr	Gly	Ser	Met	Asp	Asn
		195					200					205			
Thr	Ile	Arg	Leu	Trp	Asp	Pro	Lys	Ser	Gly	Gln	Cys	Leu	Gly	Asp	Ala
		210				215					220				
Leu	Arg	Gly	His	Ser	Lys	Trp	Ile	Thr	Ser	Leu	Ser	Trp	Glu	Pro	Ile
225					230					235					240
Leu	Val	Lys	Pro	Gly	Ser	Lys	Pro	Arg	Leu	Ala	Ser	Ser	Ser	Lys	Asp
				245					250					255	
Gly	Thr	Ile	Lys	Ile	Trp	Asp	Thr	Val	Ser	Arg	Val	Cys	Gln	Tyr	Thr
			260					265					270		
Met	Ser	Gly	His	Thr	Asn	Ser	Val	Ser	Cys	Val	Lys	Trp	Gly	Gly	Gln
		275					280					285			
Gly	Leu	Leu	Tyr	Ser	Gly	Ser	His	Asp	Arg	Thr	Val	Arg	Val	Trp	Asp
		290				295					300				
Ile	Asn	Ser	Gln	Gly	Arg	Cys	Ile	Asn	Ile	Leu	Lys	Ser	His	Ala	His
305					310					315					320
Trp	Val	Asn	His	Leu	Ser	Leu	Ser	Thr	Asp	Tyr	Ala	Leu	Arg	Ile	Gly
				325					330					335	
Ala	Phe	Asp	His	Thr	Gly	Lys	Lys	Pro	Ser	Thr	Pro	Glu	Glu	Ala	Gln
			340					345					350		

Lys Lys Ala Leu Glu Asn Tyr Glu Lys Ile Cys Lys Lys Asn Gly Asn
 355 360 365
 Ser Glu Glu Met Met Val Thr Ala Ser Asp Asp Tyr Thr Met Phe Leu
 370 375 380
 Trp Asn Pro Leu Lys Ser Thr Lys Pro Ile Ala Arg Met Thr Gly His
 385 390 395 400
 Gln Lys Leu Val Asn His Val Ala Phe Ser Pro Asp Gly Arg Tyr Ile
 405 410 415
 Val Ser Ala Ser Phe Asp Asn Ser Ile Lys Leu Trp Asp Gly Arg Asp
 420 425 430
 Gly Lys Phe Ile Ser Thr Phe Arg Gly His Ile Ala Ser Val Tyr Gln
 435 440 445
 Val Ala Trp Ser Ser Asp Cys Arg Leu Leu Val Ser Cys Ser Lys Asp
 450 455 460
 Thr Thr Leu Lys Val Trp Asp Val Arg Thr Arg Lys Leu Ser Val Asp
 465 470 475 480
 Leu Pro Gly Ile Lys Thr Lys Leu Tyr Val Asp Trp Ser Val Asp Gly
 485 490 495
 Lys Arg Val Cys Ser Gly Gly Lys Asp Lys Met Val Arg Leu Trp Thr
 500 505 510

His

<210> 4
 <211> 351
 <212> PRT
 <213> Codonanthus elegans

<220>
 <221> MOD_RES
 <222> (184)..(185)
 <223> Variable amino acid

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 Ile Leu Val Pro Val Asp Ile Ser Thr Asn Glu Leu Gln Ile Leu Cys
 20 25 30
 Asn Gln Leu Leu Gly Ser Arg Phe Cys Leu Asn Asn Glu Phe Ser Val
 35 40 45
 Ser Gly Ala Glu Ile Val Asp Ser Ile Arg Lys Ser Leu Glu Glu Ile
 50 55 60

Asp	Phe	Glu	Thr	Leu	Lys	Leu	Val	Tyr	Gln	Pro	Gln	Ala	Val	Phe	Arg	65	70	75	80
Val	Arg	Pro	Val	Thr	Arg	Cys	Ser	Ala	Ser	Ile	Pro	Gly	His	Gly	Glu	85	90	95	
Pro	Val	Ile	Ser	Ala	Gln	Phe	Ser	Pro	Asp	Gly	Arg	Gly	Leu	Ala	Ser	100	105	110	
Gly	Ser	Gly	Asp	Gln	Thr	Met	Arg	Ile	Trp	Asp	Ile	Glu	Leu	Glu	Leu	115	120	125	
Pro	Leu	His	Thr	Cys	Lys	Ser	His	Lys	Ser	Trp	Val	Leu	Cys	Ile	Ala	130	135	140	
Trp	Ser	Pro	Asp	Ala	Thr	Lys	Ile	Ala	Ser	Ala	Cys	Lys	Asn	Gly	Glu	145	150	155	160
Ile	Cys	Ile	Trp	Asn	Ala	Lys	Thr	Gly	Glu	Gln	Ile	Gly	Lys	Thr	Leu	165	170	175	
Lys	Arg	His	Lys	Gln	Trp	Ile	Xaa	Xaa	Leu	Ala	Trp	Gln	Pro	Thr	Val	180	185	190	
Lys	Met	Trp	Arg	Ala	Asp	Asp	Gly	Val	Met	Cys	Arg	Asn	Met	Thr	Gly	195	200	205	
His	Ala	His	Trp	Ile	Asn	Thr	Leu	Ala	Leu	Asn	Thr	Asp	Tyr	Ala	Leu	210	215	220	
Arg	Thr	Ser	Cys	Phe	Glu	Pro	Ser	Lys	Ile	Asn	Arg	Met	Thr	Gly	His	225	230	235	240
Met	Gln	Leu	Val	Asn	Gln	Val	Val	Phe	Ser	Pro	Asp	Thr	Arg	Tyr	Ala	245	250	255	
Ser	Ala	Ser	Phe	Asp	Lys	Ser	Val	Lys	Leu	Trp	Cys	Gly	Arg	Thr	Gly	260	265	270	
Lys	Tyr	Leu	Ala	Ser	Phe	Arg	Gly	His	Val	Gly	Pro	Val	Tyr	Gln	Val	275	280	285	
Ala	Trp	Ser	Ala	Asp	Ser	Arg	Leu	Leu	Val	Ser	Gly	Ser	Ala	Asp	Ser	290	295	300	
Thr	Leu	Lys	Val	Phe	Glu	Leu	Lys	Thr	Lys	Ser	Leu	Tyr	Tyr	Asp	Leu	305	310	315	320
Pro	Gly	His	Gly	Asp	Glu	Val	Phe	Thr	Val	Asp	Trp	Ser	Pro	Glu	Gly	325	330	335	
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<211> 103

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Leu Val Cys Asn Ala Leu Leu Ala Gln Glu Asp Pro Cys Pro Leu Ala
      20                      25                30

Phe Phe Val His Asp Ala Glu Ile Val Ser Ser Leu Gly Lys Thr Leu
      35                      40                45

Glu Ser Gln Ala Val Glu Thr Glu Lys Val Leu Asp Ile Tyr Gln Pro
      50                      55                60

Gln Xaa Leu Phe Arg Val Arg Ala Val Thr Arg Cys Thr Ser
 65                      70                75

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<210> 7
 <211> 476
 <212> PRT
 <213> *Xenopus laevis*

<400> 7

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Gly	Glu	Gly	Leu	Gly	Thr	Pro	Phe	Asp	Val	Pro	Leu	Asp	Ile	Thr	Pro	20	25	30	
Asp	Lys	Leu	Gln	Leu	Val	Cys	Asn	Ala	Leu	Leu	Gln	Glu	Glu	Asp	Pro	35	40	45	
Val	Pro	Leu	Ala	Phe	Phe	Val	Gln	Asp	Leu	Glu	Ile	Val	Thr	Ser	Leu	50	55	60	
Asp	Lys	Thr	Leu	Glu	Lys	Gln	Ser	Val	Glu	Thr	Glu	Lys	Val	Ile	Asp	65	70	75	80
Ile	Ile	Tyr	Gln	Pro	Gln	Ala	Val	Phe	Lys	Val	Arg	Ala	Val	Thr	Arg	85	90	95	
Cys	Thr	Ser	Ser	Leu	Glu	Gly	His	Thr	Glu	Ala	Val	Ile	Ser	Val	Ala	100	105	110	
Phe	Ser	Pro	Thr	Gly	Lys	Tyr	Leu	Ala	Ser	Gly	Ser	Gly	Asp	Thr	Thr	115	120	125	
Val	Arg	Phe	Trp	Asp	Leu	Ser	Thr	Glu	Thr	Pro	His	Phe	Thr	Ser	Lys	130	135	140	
Gly	His	Thr	His	Trp	Val	Leu	Ser	Ile	Ala	Trp	Ser	Pro	Asp	Gly	Lys	145	150	155	160
Lys	Leu	Ala	Ser	Gly	Cys	Lys	Asn	Ser	Gln	Ile	Phe	Ile	Trp	Asp	Pro	165	170	175	
Ser	Thr	Gly	Lys	Gln	Ile	Gly	Lys	Pro	Leu	Thr	Gly	His	Ser	Lys	Trp	180	185	190	
Ile	Thr	Trp	Leu	Cys	Trp	Glu	Pro	Leu	His	Leu	Asn	Pro	Glu	Ser	Arg	195	200	205	
Tyr	Leu	Ala	Ser	Ala	Ser	Lys	Asp	Cys	Thr	Ile	Arg	Ile	Trp	Asp	Thr	210	215	220	
Val	Met	Gly	Gln	Cys	Gln	Lys	Ile	Leu	Thr	Ser	His	Thr	Gln	Ser	Val	225	230	235	240
Thr	Ala	Val	Lys	Trp	Gly	Gly	Asp	Gly	Leu	Leu	Tyr	Ser	Ser	Ser	Gln	245	250	255	
Asp	Arg	Thr	Ile	Lys	Ala	Trp	Arg	Ala	Gln	Asp	Gly	Val	Leu	Cys	Arg	260	265	270	

Thr Leu Gln Gly His Ala His Trp Val Asn Thr Met Ala Leu Ser Thr
275 280 285

Asp Tyr Val Leu Arg Lys Gly Ala Phe Asn Pro Ala Asp Ala Ser Val
290 295 300

Asn Pro Gln Asp Met Ser Gly Ser Leu Glu Val Leu Lys Glu Lys Ala
305 310 315 320

Leu Lys Arg Ser Asn Glu Val Arg Gly Gln Gly Pro Glu Arg Leu Val
325 330 335

Ser Gly Ser Glu Asp Phe Thr Leu Phe Leu Trp Ala Pro Ala Glu Glu
340 345 350

Lys Lys Pro Leu Gln Arg Met Thr Gly His Gln Ala Leu Ile Asn Glu
355 360 365

Val Leu Phe Ser Pro Asp Thr Arg Ile Ile Ala Ser Ala Ser Phe Asp
370 375 380

Lys Ser Ile Lys Leu Trp Asp Gly Lys Thr Gly Lys Phe Leu Thr Ser
385 390 395 400

Leu Arg Gly His Val Ser Ala Val Tyr Gln Ile Ala Trp Ser Ala Asp
405 410 415

Ser Arg Leu Leu Val Ser Gly Ser Ser Asp Ser Thr Leu Lys Val Trp
420 425 430

Asp Ser Lys Thr Lys Lys Leu Leu Ile Asp Leu Pro Gly His Ala Asp
435 440 445

Glu Val Tyr Ser Val Asp Trp Ser Pro Asp Gly Gln Arg Val Ala Ser
450 455 460

Gly Gly Lys Asp Lys Cys Leu Arg Ile Trp Arg Lys
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<210> 8

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: HA epitope

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<210> 9

<211> 149

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gccacgccac atacgataca ggcgcgccca                                     149
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<210> 10
<211> 23
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Primer

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<210> 11
<211> 32
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Primer

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<222> (12)  
<223> i
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<222> (21)
<223> i
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<222> (24)  
<223> i
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<220>  
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<222> (27)  
<223> i
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<400> 11
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<220>
<223> Description of Artificial Sequence: Conserved peptide

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<210> 14
<211> 7
<212> PRT
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Primer

21

<220>
<223> Description of Artificial Sequence: Primer

21

[illegible]